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piece 1, NC\_000913, yfiF\_trxC+, config: linear, direction: +, begin: 2716521, end: 2716776

\* \* 2716530 \* \* 2716540 \* \* 2716550 \* \* 2716560 \* \* 2716570 \* \* 2716580 \* \* 2716590 \* \* 2716600  
 5' g c c g c t t a c c t t c a t t c a t c g t t c a t g c t t t c t c c a c c a g c g c g c a g a t t a c c c g a g t t c c g c g 3'  
 - ala - ala - phe - thr - phe - his - phe - ile - val - his - ala - phe - leu - his - gln - arg - cys - ala - lys - arg - ala -  
 - pro - leu - leu - pro - phe - ile - ser - ser - phe - met - leu - phe - ser - thr - ser - ala - ala - arg - ser - ala - gln - ile - thr - arg - ser - pro - lys - ser - ala -  
 - arg - phe - tyr - leu - ser - phe - his - arg - ser - cys - phe - ser - pro - pro - ala - leu - arg - glu - ala - arg - arg - leu - pro - glu - val - arg - ala -  
 ... ] NC\_000913.yifF

This figure displays a secondary structure of a tRNA gene. The structure is composed of several hairpins and loops. Key features include:

- Annotations:** The sequence is annotated with amino acid codons (e.g., \*2716610, \*2716620, \*2716630, \*2716640, \*2716650, \*2716660, \*2716670, \*2716680) and their corresponding amino acids (e.g., arg, phe, ala, met, ile, ser, tyr, gln, ser, leu, arg, leu, ser, tyr, leu, leu, asn, lys, thr, asp, cys, cys, leu, glu, gln, cys, pro).
- Color-coded regions:**
  - A purple box highlights a region from position 35 to 3.5 bits.
  - A cyan box highlights a region from position 10 to 6.3 bits.
  - A red box highlights a region from position 63 to the end of the sequence.
  - A green box highlights a region at the bottom of the structure.
- Labels:**
  - "p35 3.5 bits" is associated with the purple box.
  - "p10 6.3 bits" is associated with the cyan box.
  - "sd" (stem-loop) is labeled near the bottom right.
  - "{ ... } p35-(21)-p10 2716637 Gap 3.3 bits" is located at the bottom center.

|-----| p35-p10 2716637 total 6 5 bits

 p35 6.5 bits

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{-----} sd-(5)-ir 2716676 Gap 5.4 bits

|-----| sd-ir 2716676 yfiF\_trxC+ total 6.6 bits

{ } p35-(25)-p10 2716673 Gap 4.0 bits  
p35-p10 2716673 total 5.7 bits

p35 3.8 bit

p10 3.2 bits

-----] p35-(25)-p10 2716673 Gap 4.0 bits

3.8 bits

-25- (23) -10- 2716685 6

p35 5 6 bit

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... p35-(22)-p10 2716687 Gap  
... p35-p10 2716687 total 9.6

p35 2.9 bit

{----- ... p35-(24)-p10 2716694 Gap

2716750 \* 2716760

Genomic map of the *yfiF\_trxC+* locus. The top line shows the DNA sequence with transcription start sites marked by asterisks (\*). The bottom line shows the deduced amino acid sequence. Key features include:

- Promoters:** Promoters are indicated by red circles above the sequence.
- Open Reading Frames (ORFs):** ORFs are shown as colored boxes below the sequence. *yfiF* (red) encodes 14 codons, and *trxC* (green) encodes 18 codons.
- Start Codons:** The first codon of each ORF is highlighted in yellow.
- Stop Codons:** Stop codons are marked with red dots.
- SD Sequences:** SD sequences are shown in green boxes at the 5' end of the *trxC* gene.
- Annotations:** Below the sequence, labels indicate the amino acid sequence: fMet, pro, ile, ser, leu, leu, thr, his, pro, glu, val, ser, tyr, glu, tyr, fMet, asn, thr.

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**b10** p10 4.3 bits

[####]\_cnf\_18\_sodong

{-----} sd-(7)-ir 2716757 Gap 3.7 bits

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... ----} p35-(23)-p10 2716685 Gap 1.4 bits
... ----| p35-p10 2716685 total 6.7 bits
... -----} p35-(22)-p10 2716687 Gap 2.3 bits
... -----| p35-p10 2716687 total 9.6 bits
... -----} p35-(24)-p10 2716694 Gap 2.4 bits
... -----| p35-p10 2716694 total 6.0 bits
```

5' \* 2716770 \*  
c c g t t t g t a c c e a 3'  
- arg - leu - tyr - pro -  
- val - cys - chr -  
... NC\_000913.trxC  
... ir yfiF\_trxC+

